



**Figure S21. Comparison of peak-gene association rules.** Th17 ATAC-seq priors were constructed using different peak-gene association rules and two raw p-value cutoffs for motifs from CisBP (note that ENCODE motifs were not included in this analysis). mLASSO-StARS was run with TF mRNA or prior-based TFA at bias = .5. (Inf = infinity.)